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	1	10	20	30
NEP1-HU	MGK.....SESQMDITDINT..PKPKKKQRWTPLEI.....			SLSVLVLLL
	*	*	*	*
PEX-HUM	MEA.....ETG....SSVET..GKKANRGTRIALVV.....			FVGGLVLG
	*	*	*	*
KELL-HU	MEGHDQSEEEPRERSQAGGMGTIWSQESTPEERLPVEGSRPWAV....ARRVLTAILIL.			
	*	*	*	*
ECE1-HU	MSTYKRATLDEEDLVDSLSEGDAYPNGLQVNHFSPRSQRCWAARTQVEKRLVVLVLLA			
consens	M	T	P	L

	40	50	60	70	80	90
NEP1-HU	TIIAVTMIALYA.TYDD...GICKSSDCIKAARLIQNLMDATTEPCTDFFKYACGGWLKR					
	**	*	*	**	**	**
PEX-HUM	TILFLVSQGLLSLQAKQ...EYCLKPECIEAAAAILSKVNLSVDPDCDNFFRFACDGWISN					
	*	*	*	*	*	*
KELL-HU	.GLLLCFSVLLFYNFQNCGPRPCETSVCLDLRDHYLASGNTSVAPCTDFFSFACG...RA					
	**	*	*	*	*	*
ECE1-HU	AGLVACLAALGI.QYQTRSPSVCLSEACVSVTSSILSSMDPTVDPCHDFFSYACGGWIKA					
consens	L	L	C	C	L	V PC DFF ACGGW

	100	110	120	130	140	150
NEP1-HU	NVIPETSSRYGNFDILRDELEVVLKDVQLQEP..KTEDIVAVQAKAKALYRSCINESAIDSR					
	***	**	**	*	***	***
PEX-HUM	NPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQAKAKILYSSCMNEKAIEKA					
	*	*	**	*	**	*
KELL-HU	KETNNS.....FQELATKNKNRLRRILEVQ.NSWHPGSGEEKAFQFYNSCMDTLAIEAA					
	*	*	*	**	*	*
ECE1-HU	NPVPDGHSRWGTFSNLWEHNQAIKHLLENS.TA.SVSEAERKAQVYYRACMNETRIEEL					
consens	N	P	G F	L	LK LE	A KA Y SCMNE AIE

	160	170	180	190	200	
NEP1-HU	GGEPLLKLLPDI.YGWP..VATENWEQKYGAS.WTAEKAIQLNSKYGKKVLIINLFVGTD					
	***	*	*	*	*	
PEX-HUM	DAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPD					
	**	*	*	*	*	
KELL-HU	GTGPLRQVIEEL.....GGWRISGKWTSLNFN..RTLRLLMSQYGHFPFFRAYLGPH					
	***	*	***	*	*	
ECE1-HU	RAKPLMELIERL.....GGWNITGPWAKDNFQ..DTLQVVTAHYRTSPFFSVYVSAD					
consens	PL		G W	F	TL	Y F YV D

	220	230	240	250	260	
NEP1-HU	DKNSVNHVIHIDQPRGLPSR.DYYECTGIYKEACTAYVDFMISVARLIRQEERLPI.DE					
	***	*	*	*	*	
PEX-HUM	DKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVL.....LGA.NS					
	**	*	*	*	*	
KELL-HU	PASPHTPVIQIDQPEFDVPLKQDQEOKI.YAQIFRE.YLTYLNQLGTL.....LGG.DP					
	***	*	*	*	*	
ECE1-HU	SKNSNSNVIQVDQSGLGLPSRDYLNKTENEKVLTG.YLNYMVQLGKL.....LGGGDE					
consens	K S	VI	DQ	L LP R DY	K Y M L	LG D

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	270	280	290	300	310	320
NEP1-HU	NQLALEMNKVMELKEIANATAKPEDRNDPMLLYNKMTLAQIQNNFSLEINGKPFSLNLF					
PEX-HUM	SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMY.NKMNISELSAMIP.....QFDWLGY					
KELL-HU	SKVQEHSLSISITSRLFQFLRPLEQRRAQGKLFQMVTIDQLKEMAP.....AIDWLSC					
ECE1-HU	EAIRPQMQQILDFTALANITIPQEKRDEELIYHKVAAELQTLAP.....AINWLFP					

consens	M	E	A	P E R	K T	L	P	WL
---------	---	---	---	-------	-----	---	---	----

	330	340	350	360	370	380
NEP1-HU	TNEIMSTVNISITNEEDVVVYA....PEYLTKLKPILTKYSARDLQNLMSWRFIMDLVSS					
PEX-HUM	IKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLWWRMVYSRIPN					
KELL-HU	LQATFTPMSSLSPSQSLVWHDVEYL...KNMSQLVEEMLLKQRDFLQSHMILGLVVTLSAPA					
ECE1-HU	LNTIFYPVEINESEPIVVYDKEYL...EQISTLINT...TDRCLNNYMIWNVLVRKTSSF					

consens	V	L	L N M W	V
---------	---	---	---------	---

	390	400	410	420	430	
NEP1-HU	LSRTYKESR....NAFRKALYGT. SETATWRRCANVNGNMENAVGRLYVEAAFAGESK					
PEX-HUM	LSRRFQYRW....LEFSRVIQGTT. TLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKK					
KELL-HU	LDSQFQEARRKLSQKLRELTEQPPMPARPRWMKCVEETGFFEPTLAALFVREAFGPSTR					
ECE1-HU	LDQRFQDA....DEKFMEVMYGTTKCLPRWKFCVSDTENNLFALGPMFVKATFAEDSK					

consens	L	FQ	F	GT	P W	CV	G	FV	F	K
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	440	450	460	470	480	490				
NEP1-HU	HVVEDLIAQIREVFIQTLD. DLTWMDAETKKRAEKKALAIKERIGYPDDIVSNDNKLNN									
PEX-HUM	EMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE. FIMNDTHVNED									
KELL-HU	SAAMKLFTAIRDALITRLR. NLPWMNEETONMAQDKVAQLQVEMGASE. WALKPELARQE									
ECE1-HU	SIATEIILEIKKAFEESSL. TLKWMDEETRKSAKEKADAIYNMIGYPN. FIMDPKELDKV									
consens	L	IR AFI	L	L WMD ET	A EKA A	GYP	(4) → (1A/B) →			

	500	510	520	530	540	550			
NEP1-HU	YLENYKEDEYFENIIQNLKFSQSCKQLKKLREKVDKDEWISGAAVVNAFYSSGRNQIVFP								
PEX-HUM	LKAIFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFP								
KELL-HU	YND.IQLGSSFLQSVLSCVRSLRARIIVQSFLQPHPQHRWKVSPWDVNAYYSVSDHVIVFP								
ECE1-HU	FNDYTAVPDLYFENAMRFFNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPTKNEIVFP								
consens	YF N		LR	W	P	VNA YS	N	IVFP	(2A/B)

~~1~~ 1 (cont'd)

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	560	570	580	590	600	610
NEP1-HU	AGILQPPFFSAQQ.	SNSLNYYGGIGMIGHEITHGFDDNGRNFNKGDLVDWWWTQQSASNF				
PEX-HUM	AGELOQKPFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWSTSEEKF					
KELL-HU	AGLLQPPFFHPGY.	PRAVNFGAAGSIMAHELLHIFYQL...LLPGGCL.....ACDNHAL				
ECE1-HU	AGILQAPFYTRSS.	PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWKNSSVEAF				
consens	AG LQ PFF	P LN G IG	GHE TH FD	GR	K G L WW	S F

	620	630	640	650	660	670
NEP1-HU	KEQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGL			5QAYRAYQNYI..KKNG.EE		
PEX-HUM	KEKTKCMINQYSNYYWK.	KAGLNVKGKRTLGENIADNGGL	R	REAFRAYRKWINDRRQGLEE		
KELL-HU	QE AHLCLKRHYAAF..	PLPSRTSFNDSLTLGENIADNGGL	E	AADVVGGLAIALQAYSKRL..LRHH.GE		
ECE1-HU	KRQTECMVEQYSNY..	SVNG.EPVNGRHTLGENIADNGGL	A	AAAYRAYQNWV..KKNG.AE		
consens	KE CM QY N	NG	TLGENIADNGGL	(3)	A RAY	G E

	680	690	700	710	720	730
NEP1-HU	KLLPGLDLNHKQLFFLNFAQVWCCTYRPEYAVMSIKTDVHSPGNFRIIGTLQNSAEFSEA					
PEX-HUM	PLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPQFRVNGAISNFEFQKA					
KELL-HU	TVLPSLDLSPQQIFFRSYAQVMCRKPSQDSH....	DTHSPPHLRVHGPLSSTPAFARY				
ECE1-HU	HSLPTLGLTNNQLFFLGFAQVWCVRTPESSHEGLITDPHSPSRFRVIGSLSNSKEFSEH					
consens	LP L L	QLFFL	AQV C	PE	D HSP	FRV G LSN EF

	740	750	
NEP1-HU	FHCRKNNSYM	NPEKK.CRVW	
PEX-HUM	FNCPPNSTMN	RGMDSCLRW	
KELL-HU	FRCARGALLNPSSR.	CQLW	
ECE1-HU	FRCPPGSPMNPPHK.	CEVW	
consens	F C	S MNP	C W

~~7-1~~ 1 (cont'd)

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PRIMER	SEQUENCE
(1A)	5'-TGGATGGAT/CGA/CIGG/AIACIA/CA-3'
(1B)	5'-TGGATGGAT/CGA/CIGG/AIACIA/CG-3'
(2A)	5'-A/GTIGTITTT/CCCIGGGIA/GT/AIC/TTA/TCA-3'
(2B)	5'-A/GTIGTITTT/CCCIGGGIA/GT/AIC/TTG/CCA-3'
(3)	5'-AIIICCCIA/TC/TA/GTCIGGIG/ACTA/GTTT/CTTC-3'
(4)	5'-GAT/CAAAT/CTIGAT/CGAA/GT/CTAAAT/CTGGATGG-3'
(5)	5'-T/CT/ACCAIACT/GA/GCATCG/TT/CTTCATGGG/ATG-3'

FIGURE - 2

## Sequence of NL-1 cDNA from mouse

met val glu arg ala gly trp cys arg lys ser pro gly phe val glu tyr gln leu met val leu leu leu gln ala  
 1 ATG GAG AGA GCA GGC TGG TGT CGG AAG TCC CCA GGC TAC GAG TAT GGG CTG GTC ATG GTG CTG CTG CTG CTG CTG CTG GCA GCC  
 ille val thr leu gly val phe tyr ser lle gly lys gln leu pro leu leu ser leu leu his phe ser trp asp glu arg thr val  
 91 ATA GTG ACT CTC GGT GTC TCC TAC AGC ATA GGG AAG CAG CTG CCC CTC TCA ACT AGC CTG CTA CAC TCC TCC TGG GAT GAG AGG ACG GTC  
 val lys arg ala leu arg asp ser leu lys ser asp lle cys thr thr pro ser cys val lle ala ala arg lle leu glu asn  
 181 GTC AAA CGA GCC CTC AGG GAT TCA TCA TCA TCG AAA AGT GAC ATC TGC ACC ACC CCA ACC TGT GTG ATA GCA GCT GCC AGA ATC CTC GAA AAC  
 met asp gln ser arg asn pro cys glu asn phe tyr gln tyr ala cys gln gln trp leu arg his val lle pro glu thr asn ser  
 271 ATG GAC CAA TCG AGG AAC CCC TGT GAA AAC TTC TAC CAG TAC GGC TGG CTG AGG CAC CTC GTC ATC CCA GAG ACC AAC TCC  
 arg tyr ser val phe asp lle leu arg asp glu leu glu val lle leu lys gln val leu glu asp ser thr ser gln his arg pro ala  
 361 CGA TAC AGC GTC TTT GAC ATC CTG CGG GAC GAG CTG GAG GAT TCC ACT TCC CAG CAT CGC CCG CTC ACT TCC CAG CAT CGC CCG GCC  
 val glu lys ala lys thr leu tyr arg ser cys met asn gln ser val lle gln lys arg asp ser glu pro leu leu ser val leu lys  
 451 GTG GAG AGG GCC AAG ACA CTA TAT CGC TCC TGG ATG AAC CAA AGT GTG ATC GAG AAG AGA GAC TCT GAG CCC CTG CTG AGC GTC TTA AAA  
 met val gln gln trp pro val ala met asp lys trp asn glu thr met gln leu lys trp glu leu glu arg gln leu ala val leu asn  
 541 ATG GTC GGA GGT TGG CCA GGT GCC ATG GAT AAG TGG AAC GAG ACC ATG GGC CTC AAG TGG GAA CTG GAG CGA CAG TTG GCT GTG TTG AAC  
 ser gln phe asn arg arg val lle asp leu phe lle trp asn asp asp gln asn ser ser arg his val lle tyr lle asp gln pro  
 631 TCG CAG TTC AAC AGG CGG GTC CTC ATC GAC CTC ATC GAC CTC ATC GAC GTC TAC TGG AAT GAC GAC CAG AAC TCC AGC CGG CTC ATC TAC TAC ATA GAC CAG CCC  
 thr leu gln met pro ser arg glu tyr tyr phe gln glu asp asn asn his lys val arg lys ala tyr leu gln phe met thr ser val  
 721 ACC TTG GGC ATG CCA TCC CGG GAG TAC TAT TTC CAG GAG AAC AAC CAC AAG GTC CGG AAA GCC TAC CTG GAG TTC ATG ACG TCA GTC

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THE - 3 (cont'd)

## Sequence of NL-2 cDNA from humans

1 met val glu ser ala gly arg ala gly gln lys arg pro gly phe leu glu leu leu leu leu val 28  
 1 GTG GGG ATG GTG GAG AGC GCC GGG CGC CGT GCA GGG CAG AAC CGC CCG GGG TTC CTC GAG GGG CTG CTG CTG CTG CTG CTG CTG GTC ACC  
 ala ala leu val ala leu gly val leu tyr ala asp arg arg gly lys gln leu pro arg leu ala ser arg leu cys phe leu gln glu 58  
 91 GCT GCC CTG GTG GCC TTC GTC CTC TAC GCC GAC CGC AGA GGG AAG CAG CTG CCA CGC CTR GCT AGC CGG CTG TGC TTC TTA CAG GAG  
 glu arg thr phe val lys pro arg gly ile pro glu ala gln glu val ser glu val cys thr pro gly cys val ile ala 88  
 181 GAG AGG ACC TTT GTA AAA CGA AAA CCC CGA GGG ATC CCA GAG GTC AGC GAG GTG AGC GTC GTC ACC ACC CCT GGC TGC GTG ATA GCA  
 ala ala arg ile leu gln asn met asp pro thr thr glu pro cys asp asp phe tyr gln phe ala cys gly gly trp leu arg arg his 118  
 271 GCC GCG AGG ATC CTC CAG AAC ATG GAC CCG ACC ACG GAA CCG TGT GAC GAC GAC TAC CAG TTT GCA TGC GGA TGG CTG CGG CGC CAC  
 val ile pro glu thr asn ser arg tyr ser ile phe asp val leu arg asp glu val glu val lys ala val leu glu asn ser 148  
 361 GTG ATC CCT GAG ACC AAC TCA AGA TAC AGC ATC TTT GAC GTC CTC CGC GAC GAG CTG GAG GTC GTC AAA GCG GTG CTG GAG ATA TCG  
 thr ala lys asp arg pro ala val glu lys ala arg thr leu tyr arg ser cys met asn gln ser val ile glu lys arg gly ser gln 178  
 451 ACT GCC AAG GAC CGG CCG GCT GTG GAG AGC ACG TCC TAC CGC ATG AAC CAG AGT GTG ATA GAG CAG GTC TCT CAG  
 pro leu leu asp ile leu glu val val gln gly trp pro val ala met asp arg trp asn glu thr val gln leu glu trp glu leu glu 208  
 541 CCC CTG CTG GAC ATC TTT GAG GTG GTC GGC TGG CCG GTG GCA GGG ATG GAC AGG AAC GAG ACC GTA GGA CTC GAG TGG GAG CTG GAG  
 arg gln leu ala leu met asn ser gln phe asn arg val leu ile asp leu phe ile trp asn asp gln asn ser ser arg his 238  
 631 CGG CAG CTG GGG CTG ATG AAC TCA CAG TTC AAC AGC GTC CTC ATC GAC CGC GTC ATC TGG AAC GAC GAG AAC TCC AGC CGG CAC  
 ile ile tyr ile asp gln pro thr leu gly met pro ser arg glu tyr tyr phe asn gln gly ser asn arg lys val arg glu ala tyr 268  
 721 ATC ATC TAC ATA GAC CAG CCC ACC TTG GGC ATG CCC TCC CGA GAG TAC TAC TTC AAC GGC AGC AAC AAG GTG CGG GAA GCC TAC  
 leu gln phe met val ser val ala thr leu arg glu asp ala asn leu pro arg asp ser cys leu val gln glu asp met val gln 298  
 811 CTG CAG CTG ATC TTC GTC GAC AGC GTG TCA GTC CGG GAG GAT GCA AAC CTG CCC AGG GAC AGC TGC GTG CAG GAC GAC AGC ATG GTG CAG

— 4 —

val leu glu leu glu thr gln leu ala lys ala thr val pro gln glu glu arg his asp val ile ala leu tyr his arg met gly leu  
 901 GTT CTG GAG CTC GAG ACA CAG CTG GAG GCC CTC GAG ACG AAG GCC ACG CTC GTC GAC GTC ATC CAC CGG ATG GGA CGA CAC GAC GTC ATC CGG TTG TAC CTC GAC CGG AGA CAA ACT GTG CTC ATA CAA ACT GTG CTC TCT GTC AAA ATC AAG CTG CTG 358

glu glu leu gln ser gln phe gly leu lys gly phe asn trp thr leu phe ile gln thr val leu ser ser val lys ile lys leu leu  
 991 GAG GAG CTG CAA AGC CAG TTT GGC CTC AAC TGG ACT CTG TGG ACT AAC TGG ACT CTG TAC AAC AAC CTT GAA AAC AAC CTC CAG AAC ATC ATC GAC ACC TAC TCA GCC AGG ACC ATA CAG AAC 388

Pro asp gln glu val val val tyr gly ile pro tyr leu gln asn leu glu asn ile asp thr tyr ser ala arg thr ile gln asn  
 1081 CCA GAT GAG GAA GTC GAG GTG GTG GTC GTC TAT GGC ATC CCC TAC CTC CAG AAC AAC CTT GAA AAC AAC CTC CAG AAC ATC ATC GAC ACC TAC TCA GCC AGG ACC ATA CAG AAC 418

tyr leu val trp arg leu val val asp arg ile gln ser leu ser gln arg phe lys asp thr arg val asn tyr arg lys ala leu phe  
 1171 TAC CTG GTC TGG CGC CTC GTC GAG 448

gly thr met val glu val arg trp arg glu cys val gly tyr val asn ser asn met glu asn ala val gly ser leu tyr val arg  
 1261 GGC ACA ATG GTC GAG GAG GTC GTC GAG GTC GTC GAG AAC AAC ATG GAG AAC AAC GTC AAC ATG GAG AAC AAC GTC GTC GTC GTC GAG 478

glu ala phe pro gly asp ser lys ser met val arg glu leu ile asp lys val arg thr val phe val glu thr leu asp glu leu gly  
 1351 GAG GCG TTC CTC GCA GAC AGC ATG GTC ATT GAC AAG GTG CGG ACA GTG CCTG GAG ACC CTG GAC GAG CTG GTC GTC GGC 508

trp met asp glu glu ser lys lys ala gln glu lys ala met ser ile arg glu gln ile gly his pro asp tyr ile leu glu glu  
 1441 TGG ATG GAC GAG TCC AAC AAG AAC GTC ATT GAC AAG GTG CGG CGG CGG CGG CGC ATC CGG CGG CGC CCT GAC TAC ATC CTG GAG GAG 538

met asn arg arg leu asp glu glu tyr ser asn leu asn phe ser glu asp leu tyr phe glu asn ser leu gln asn leu lys val gly  
 1531 ATG AAC AGC CGG CGC CTG GAC GAG TAC TCC ATT CTG AAC TGT TCA GAG GAC CTG TAC ATT GAG AAC CTC AAC ATG GTC GGC 568

ala gln arg ser leu arg lys leu arg glu lys val asp pro asn leu trp ile ile gly ala val val asn ala phe tyr ser pro  
 1621 GGC CAG CGG AGC CTC AGG AAG CTT CGG GAA AAC GTG GAC CTC AAC TGG ATC ATC GGG GCG GCG GTC AAT GCG TTC TAC TCC CCA 598

asn arg asn gln ile val phe pro phe pro phe ser lys glu gln pro gln ala leu asn phe gly gly ile  
 1711 AAC CGA AAC AAC CAG ATT GTA TTC CCT GCC GGG ATC CTC CAG CCC CCC TTC AGC AAG GAG CAG CCA CAG GCC TGT AAC TTT GCA GGC ATT 628

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~~FIGURE 4~~ - 4 (cont'd)

gly met val ile gly his glu ile thr his gly phe asp asp asn gly arg arg phe asp lys asn met met asp trp trp ser  
 1801 GGG ATG GTG ATC GGG CAC GAG ATC ACG CAC GGC TTT GAC GAC ATT GGC AAC ATG GAT TGG TGG AGT  
 asn phe ser thr gln his phe arg glu gln ser glu cys met ile tyr gln tyr gln tyr ser trp asp leu ala asp glu gln asn  
 1881 AAC TTC TCC ACC CAG CAC TGC TCC CGG GAG TCA GAG TAC ATG ATC TAC GAC TAC GAC AAC ATG GAT TGG TGG GAC CTC GCA GAC AAC  
 val asn gly phe asn thr leu gln glu asn ile ala asp asn gln tyr val arg gln ala tyr lys ala tyr leu lys trp met ala glu  
 1981 GTG AAC GGA TTC AAC ACC CTT GGG GAA AAC ATT GCT GAC AAC ATT GCT GAC AAC GCA GGG GAG CCG CAA GCC TAT AAG GCC TAC CTC RAG TGG ATG GCA GAG  
 gly gly lys asp gln leu pro gly leu asp leu thr his glu gln leu phe phe ile asn tyr ala gln val trp cys gly ser tyr  
 2071 GGT GGC AAC GAC CAG CTG CCC GGC CTG GAT CTC ACC CAT GAG CAG CTC TTC ATC AAC TAT GCC CAG GGG TGC GGG TCC TAC  
 arg pro glu phe ala ile gln ser ile lys thr asp val his ser pro leu lys tyr arg val leu gly ser leu gln asn leu ala ala  
 2161 CGG CCC GAG TTC GGC ATC CAA TCC ATC AAG ACA GAC GTC CAC AGT CCC CTG AAG TAC AGG GTC CGG TCG CAG AAC CTG GCC GGC  
 phe ala asp thr phe his cys ala arg gly thr pro met his pro lys glu arg cys arg val trp ter  
 2251 TTC GCA GAC ACC TGC CAC TGT GCC CGG GGC ACC CCC ATG CAC CCC AAG GAG CGA TGC CGC GTG TGG TAG CCA AGG CCC TGC CGC GCT GTG  
 2341 CGG CCC ACG CCC ACC CGC TGC TCG GAG GCA TCT GTG CGA AGG TGC AGC TAG CGG CGA CCC AGT GTC CGT CCC GCC CCC AAC CAT GCC  
 2431 AAG CCT GCC TGC CAG GCC TCT GCG CCT GGC CTA GGG TGC AGC CAC CTG CCT GAC ACC CAG GGA TGA GCA GTG TCC AGT GCA CCT GGA  
 2521 CCG GAG CCC CCT TCA CAG ACA CCC GCG GGG CTC AGT GGC CCC GTC ACA ACT CTG TAG AGA CAA TCA ACT GTG TCC CCA CCC TTC AAG  
 2611 GTG CAT TGT CTT CCA GTC TCT ACA GCT TCA GAA CTT GAG CTA AGT AAA TGC TTT CAA AGA AAA AAA

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## Sequence of NL-3 cDNA from human

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355  
 ile thr val ser glu tyr asp asp leu arg arg asp val ser ser met tyr asn lys val thr leu gly 9ln 1eu gln lys ile thr pro  
 1171 ATC ACT GTG TCA GAG TAT GAC GAC CTA CGG CGA GAT GTC AGC TCC ATG TAC AAC AAG GTG ACG CTC GAG CTC GAG CCC  
 382  
 his leu arg trp lys trp leu leu asp gln ile phe gln glu asp phe ser glu glu glu val val leu ala thr asp tyr met  
 1261 CAC TTG CCG TGG AAG TGG CTC CTA GAC CAG ATC TTC CAG GAG GAC TTC TCA GAG GAA GAG GCG ACA GAC TAC ATG  
 412  
 gln gln val ser gln leu ile arg ser thr pro his arg val leu his asn tyr leu val trp arg val val val leu ser glu his  
 1351 CAG CAG TCG TCG CAG CTC ATC CGC TCC ACA CCC CAC CTC CAG GTC CTC CAC AAC TAC CTC GTG TGG CGC GTC CTG AGT GAA CAC  
 442  
 leu ser pro pro phe arg glu ala leu his glu leu ala gln glu met glu gly ser asp lys pro gln glu leu ala arg val cys leu  
 1441 CTG TCC CCG CCA TTC CGT GAG GCA CTC GAG CTC GCA CAG GAC ATG GAG GGC AGC AAC CCA CAG GAG CTG GCC CCG GTC TGC TTG  
 472  
 gln gln ala asn arg his phe gly met ala leu gly ala leu phe val his glu his phe ser ala ala ser lys ala lys val gln gln  
 0 1531 GGC CAG GCA AAT CGC CAC TTT GGC ATG GCG CTC TTT GGC GCC CTC TCA GCT GCA CAC TAC GAG CAC TGT GCA CAG CAG GAG  
 502  
 leu val glu asp ile lys tyr ile leu gly gln arg leu glu glu leu app tpp met asp ala glu thr arg ala ala arg ala lys  
 1621 CTA GTG GAA GAC ATC AAG TAC ATC CGT GGC CAG CTC GAC GTC GAG CTC GAG CTC GAG GAC ACC AGC GCT GCT GCT GCG GGC AAG  
 532  
 leu gln tyr met met val met val gly tyr pro asp phe leu leu lys pro asp ala val asp lys glu tyr glu pho glu val his glu  
 1711 CTC CAG TAC ATG ATG GTG ATG GTC GGC TAC CCG GAC TTC CTG AAA CCC GAT GCT GTG GAC AAG GAC TAT GAG TTT GAG GTC CAT GAG  
 562  
 lys thr tyr phe lys asn ile leu asn ser ile arg phe ser ile gln leu ser val lys lys ile arg gln glu val asp lys ser thr  
 1801 AAC ACC TAC TTC AAC AAC ATC TTG AAC AGC ATC CGC TTC AGC ATC CAG CTC TCA GTC AAC AAG ART CCC CAG GAG GTC GAC AAG TCC AGC  
 592  
 tpp leu leu pro pro gln ala leu asn ala tyr tyr leu pro asn lys asn gln met val phe pro ala gly ile leu gln pro thr leu  
 1891 TGG CTC CTC CCC CCA CAG GCG CTC AAC TAC TAT GTC AAC AAC CAG AAC CTC ATG GTC TTC CCC GCG GGC ATC CTC CAG CCC ACC ATG  
 622  
 tyr asp pro phe pro gln ser leu asn tyr gly gly ile gly thr ile ile gly his glu leu thr his gly tyr asp asp tpp gly  
 1981 TAC GAC CCT GAC TTC CCA CAG TCT CTC AAC TAC GGC GGC ATC ACC ATC ATT GGA CAT GAG GTC ACC CAC GGC TAC GAC GAC TGG GGG  
 652

7 is 5 (cont'd)

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gly gln tyr asp arg ser gln asn leu leu his trp trp trp glu ala ser tyr ser arg phe leu arg lys ala glu cys ile val arg  
2071 GGC CAG TAT GAC CGC TCA GGG AAC CTG CTC CAC TGG TGG ACG GAG GCC TCC TAC ACC CGC TTC CTC CGA AAG GCT GAG TGC ATC GTC CGT  
leu tyr asp asn phe thr val tyr asn gln arg val asn gly lys his thr leu gln glu asn ile ala asp met gly gln leu lys leu  
2161 CTC TAT GAC AAC TTC ACT GTC TAC AAC CAG CCG GTG AAC GGG CTT ACG CTC GAG AAC ATC GCA GAT ATG GGC GGC CTC AAC CTC AAG CTC  
ala tyr his ala tyr gln lys trp val arg glu his gly pro glu his pro leu pro arg leu lys tyr thr his asp gln leu phe phe  
2251 GCC TAC CAC GCC TAT CAG AAC TGG GTG CCG GAG CAC CGC CCA CTC GAG CAC CAC CTC AAG TAC ACA CAT GAC CTC GTC CTC TAC  
ile ala phe ala gln asn trp cys ile lys arg arg ser gln ser ile tyr leu gln val leu thr asp lys his ala pro glu his tyr  
2341 ATT CCC TTG GCC CAG AAC TGG TGC ATC AAG CGG CCG TCG CAG TCC ATC TAC TAC TAC CTC CAG GTG ACT GAC AAC CAT GCC CCT GAG CAC TAC  
arg val leu gly ser val ser gln phe glu glu phe gly arg val leu his cys pro lys val ser pro met asn pro ala his lys cys  
2431 AGG GTG CGC AGT GTG TCC CAG TTT GAG GAG TTT GGG CGG GTT TTA CAC TGT CCA AAC GTC TCA CCC ATG AAC CCT GGC CAC AAG TGT  
775 ser val trp ter  
2521 TCC GTG TGG TGA CCC TGG CTG CCC GCC TGC ACG CCC CCA CTG CCC CCG CAC GAA TCA CCT CCT GCT GGC TAC CGG GGC AGG CAT GCA CCC  
2611 GGT GCC AGC CCC GCT CTG CGC ACC ACC TGC CTT CCA GCC CCT CCA GGA CCC GGT CCC CCT GCT GCC CCT CAC TTC AGG AGG GGC CTG GAG  
2701 CAG GGT GAG GCT GGA CTT TGG GGG GCT GTG AGG GAA ATA TAC TGG GGT CCC CAG ATT CTG CTC TAA GGG GGC CAG ACC CTC TGC CAG GCT  
2791 GGA TTG TAC GGG CCC CAC CTT CGC TGT GTT CTT GCT GCA AGT CTG GTC AAA TAA ATC ACT GCA CTG TTA AAA AAA AAA AAA

7 - 5 (cont'd)

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## Sequence comparison between NEP, NL1, NL2 and NL3

	1	10	20	30	40
NEP-HUM	MG.....	KSESQMDITDINTPKPKKKQRWTPLEISLSVLVLL..	LTII...	AV	
	*		*	*	*
NL1-MOU	MV.....	ERAGWCRKKSPGFVEYGLMVL	LLLLLGAIVTLG.V..	FYSI.GKQL	
	**	**	***	***	****
NL2-HUM	MV.....	ESAGRAGQKRPGFLEGGL	LLLLLVAALVALGVL..	YADRRGKQL	
	*		*	*	***
NL3-HUM	MEPPYSLTAHYDEFQEVKYVSRCGAGGARGASLPPG	FPLGAARSATGARSGL	PRWNRRREV		

	50	60	70	
NEP-HUM	TMIA.....LYATYDD.....	GICKSSDCI	KAARLIQ.NMDATT	
	*	*	**	***
NL1-MOU	PLTLSL.....LHFSDERTVVKR...	ALRDSSLKSDICTTPSCVIAAARILE.NMDQSR		
	***	**	***	***
NL2-HUM	PRLASR.....LCFLQEERTFVKRKPRGIPEAQEVSEVCTTPGCVIAAARILQ.NMDPTT			
	*	**	*	***
NL3-HUM	CLLSGLVFAAGLCAILAAMLALKYLG	PVAAGGGACPEGC	PERKAFARAARFLAANLDASI	

	80	90	100	110	120	130
NEP-HUM	EPCTDFFKYACGGWLKRNVIPETSSRYGNFDILRDELEVVLKDV	LQEPKTEDIVAVQ.KA				
	***	*****	***	*****	***	**
NL1-MOU	NPCENFYQYACGGWLRRHVI	PETNSRYSVFDILRDELEVILKG	VLEDSTSQHRPAVE.KA			
	**	***	*****	***	***	***
NL2-HUM	EPCDDFYQFACGGWLRRHVI	PETNSRYSIFDVLRDELEVILKAVLENSTAKDRPAVE.KA				
	***	*****	***	***	***	***
NL3-HUM	DPCQDFYSFACGGWLRRHAI	PDDKLTYGTIAAIGEQNEERL	RRLLARP	GGGGPGGAAQRKV		

	140	150	160	170	180	190
NEP-HUM	KALYRSCINESAIDSRGGEPLL	KLLPDIY	GWPVATENWEQKY	GASWTAEK	AIAQLNSKYG	
	*****	*	***	*	*	***
NL1-MOU	KTLYRSCMNQSVIEKRDSEPLL	SVLKMVG	GPVAMDKWNETMGLK	WELERLQ	AVLNSQFN	
	*****	***	*****	***	*****	***
NL2-HUM	RTLYRSCMNQSVIEKRGSQPLLDI	LEVVG	GPVAMDRWNETVG	LEWELERLQ	LALMNSQFN	
	***	**	***	***	***	***
NL3-HUM	RAFFRSCLDMREIERLG	PRPMLEVIEDCGG	WDLGGA	ERPGVAAR	WDLNRLYKAQGVYS	

	200	210	220	230	240	250
NEP-HUM	KKVLINLFVGTDDKNSVN	HVIIDQ	PRGLPSRDYY	ECTGIY	KEACTAY	VDFMISVARLI
	***	**	***	***	**	***
NL1-MOU	RRVLIDLFIWNDDQNS	NRHVIYIDQ	PTLGMP	SREYYFQEDNN	HKVRKAYLE	FMTSVATML
	*****	*****	*****	*****	***	*****
NL2-HUM	RRVLIDLFIWNDDQNS	RHIIYIDQ	PTLGMP	SREYYFNGGS	NRKVREAYLQ	FMVSATLL
	***	**	***	***	***	***
NL3-HUM	AAALFSLTVSLDDRN	SSRYVIRIDQ	DGLTL	PERTLYLAQ	DEDSE..	KVLAAYRVFMERVL

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	260	270	280	290	300	310
NEP-HUM	RQEERLPIDENQLALEMNKVMELEKEIANATAKP..	EDRNDPMILLYNKMTLAQIQNNFSL				
	*	*	***	***	*	*
NL1-MOU	RKDQNLSKESAMVREEMAEVLELETHLANATVPQ..	EKRHDVTALYHRMDLMELQERFGL				
	*	*	*	*****	*	***
NL2-HUM	REDANLPRDSCLVQEDMVQVLELETQLAKATVPQ..	EERHDVIALYHRMGLEELQSQFGL				
	*	*	*	***	*	***
NL3-HUM	SL...LGADAV..EQKAQEILQVEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQKITP.					

	320	330	340	350	360	370
NEP-HUM	EINGKPFSWLNFTNEIMSTVNISITNEEDVVVYAPEYLTKLPILTYSARDLQNLMSWR					
	*	*	*	*****	*	***
NL1-MOU	...KGFNWTLFIQNVLSSVEVELFPDEEVVVYGIPIYLENLEDIIDSYSARTMQNYLVWR					
	*****	*****	*	*****	*	*****
NL2-HUM	...KGFNWTLFIQTVLSSVKIKLLPDEEVVVYGIPIYLNLENIIDTYSARTIQNYLVWR					
	*	*****	*	*	*	*****
NL3-HUM	...HLRWKWLDDQIF...QEDFSEEEEVVLLATDYMQQVSQLIRSTPHRVLHNYLVWR					

	380	390	400	410	420	430
NEP-HUM	FIMDLVSSLRTYKESRNAFRKALYGTSETATWRRCANVNGN MENAVGRLYVEAAFAG					
	*	***	**	*****	*	***
NL1-MOU	LVLDRIGSLSQRFKEARVDYRKALYGTTEEVRWREC VS YVN SNM EAVGSLYIKRAFSK					
	*****	*****	*	*****	*****	*****
NL2-HUM	LVLDRIGSLSQRFKDTRVNYRKALFGTMVEEV RWREC VGYVN SNM EAVGSLYVREA FPG					
	*	**	*	*	*	***
NL3-HUM	VVVVLSEHLSPPFREALHELAQEMEGSDKPQELARVCLGQANRHFGMALGALFVHEHFS A					

	440	450	460	470	480	490
NEP-HUM	ESKHVVEDLIAQIREVFIQTLDDL TWMDAETKKRAE EKALAIKERIGYPDDIVSNDNK.L					
	**	*	**	**	***	**
NL1-MOU	DSKSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQE KAMNI REQIGYPDYILEDNNKHL					
	*****	*****	*	*****	*****	*****
NL2-HUM	DSKSMVRELI D KVRTVFETLDELGWMDEESKKKAQE KAMSIREQIGHPDYILEEMNRRL					
	**	*	*	*	*	*
NL3-HUM	ASKAKVQQLV EDIKYI LGQRLEELDWMDAETRAA RAKLQYMM MVGYPDFLLKPDA..V					

	500	510	520	530	540	550
NEP-HUM	NNEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWI SGAAV VNAFYSSGRNQI					
	**	*	***	*****	***	*****
NL1-MOU	DEEYSSLTFYEDLYFENG LQNLKNN AQRSLKKLREKVDQNLWIIGAAV VNAFYSPRNQI					
	*****	*	*****	*****	*****	*****
NL2-HUM	DEEYSNLNFSEDLYFENS LQNLKVG AQRSLRK LREKVDPNLWIIGAAV VNAFYSPRNQI					
	*	*	**	*	*	**
NL3-HUM	DKE. YEFEVHEKTYFKNILNSIRFSIQLSVKKIRQEVDKSTWLPPQALNAYYLPNKNQM					

~~7-8~~ - 6 (cont'd)

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	560	570	580	590	600	610
NEP-HUM	VFPAGILQPPFFSAQQSNSLNYYGGIGMVIGHEITHGFD	DDNGRN	FNFKDGD	LVDWW	TQQSAS	
	*****	***	*****	*****	***	***
NL1-MOU	VFPAGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFD	DDNGRN	FDKNG	NMLDWW	SNFSAR	
	*****	***	*****	*****	***	***
NL2-HUM	VFPAGILQPPFFSKEQPQALNFGGIGMVIGHEITHGFD	DDNGRN	FDKNG	NMM	DWW	SNFSTQ
	*****	***	***	***	***	***
NL3-HUM	VFPAGILQOPTLYDPDFPQSLNYYGGIGTIIGH	ELTHGY	DDWGGQY	DRSGN	LLHWW	TEASYS

	620	630	640	650	660	670	
NEP-HUM	NFKEQSQC	MVYQYGNF	SWDLAGGQH	LN	INTLGENI	ADNGGLGQAYRAYQNYIKKN	
	*****	*****	*****	***	*****	***	
NL1-MOU	HFQQQSQC	MIYQYGNF	SWELADN	QN	VNGF	STLGENI	ADNGGVRQAYKAYL
	***	***	***	***	***	***	RWLADGGKDQ
NL2-HUM	HFREQSEC	MIYQYGN	YSWDLADE	EQN	VNGF	NTLGENI	ADNGGVRQAYKAYL
	***	***	***	***	***	***	KWMAEGGKDQ
NL3-HUM	RFLRKAECIV	RLYDN	FT...	VYNQRV	NGKHTL	GENIADM	GGKLAYHAYQK
	*****	*****	***	*****	*****	*****	WVREHGPEH

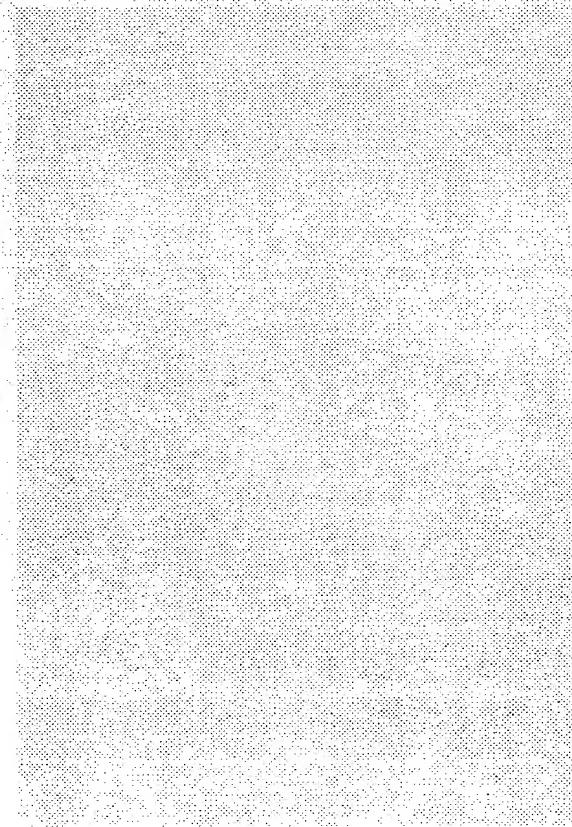
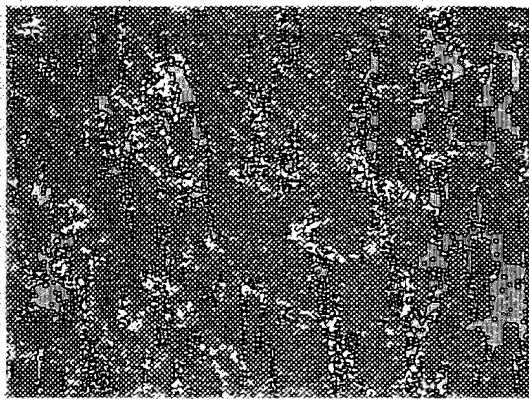
	680	690	700	710	720	730
NEP-HUM	LLPGLDLN	HQQLFFLN	FAQVWC	GTYRPE	YAVNSIK	TDVHSPGN
	***	***	***	***	***	***
NL1-MOU	RLPGLNL	TYAQLFF	FINYAQVWC	CGSYRPE	FAVQSI	KTDVHSPL
	***	***	***	***	***	***
NL2-HUM	QLPGLDL	THEQLFF	FINYAQVWC	CGSYRPE	FAIQSI	KTDVHSPL
	***	***	***	***	***	***
NL3-HUM	PLPRL	KYTHDQLFF	IAFAQ	NWC	IKRRSQSI	YLQVLT
	*****	*****	***	***	***	***

	740	750	
NEP-HUM	HCRKNSYM	NPEKKCRVW	
	**	***	
NL1-MOU	HCPRGSPM	HPMKRCRIW	
	***	***	
NL2-HUM	HCARGTPM	HPKERCRIW	
	**	***	
NL3-HUM	HCPKVSPM	NPAHKCSVW	

~~7-10~~ (cont'd)

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# NL1 in the TESTIS



===== 7

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## Expression of PEX and NL-3 in normal and Hyp mouse embryos

PEX

PEX

NL-3

NL-3

Hyp

N

Hyp

N

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# NL3 in the BRAIN

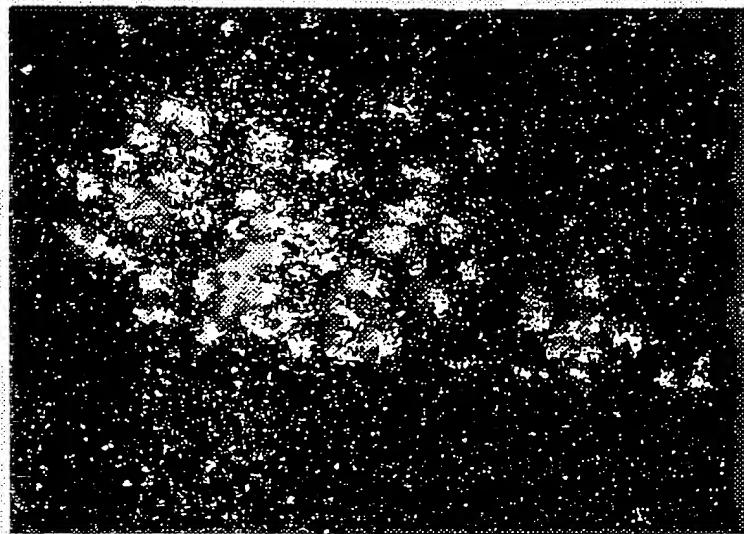
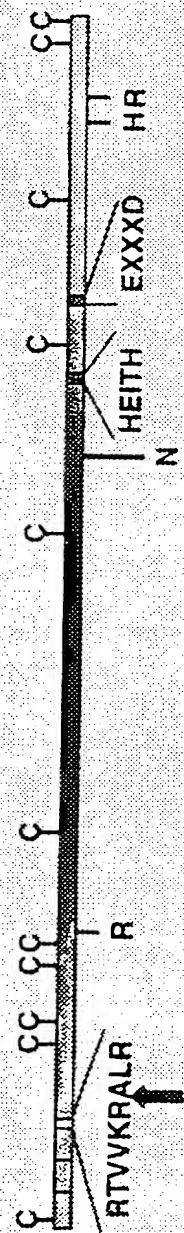


FOTO 280 - ENSETE 600

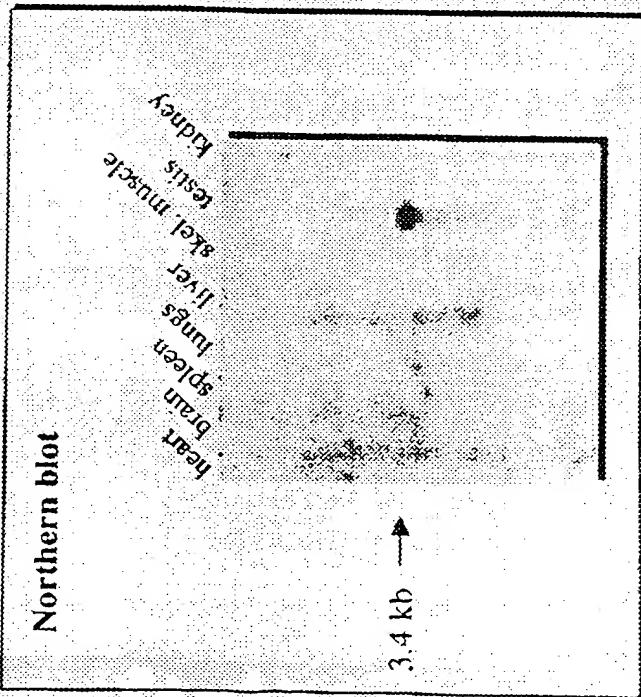
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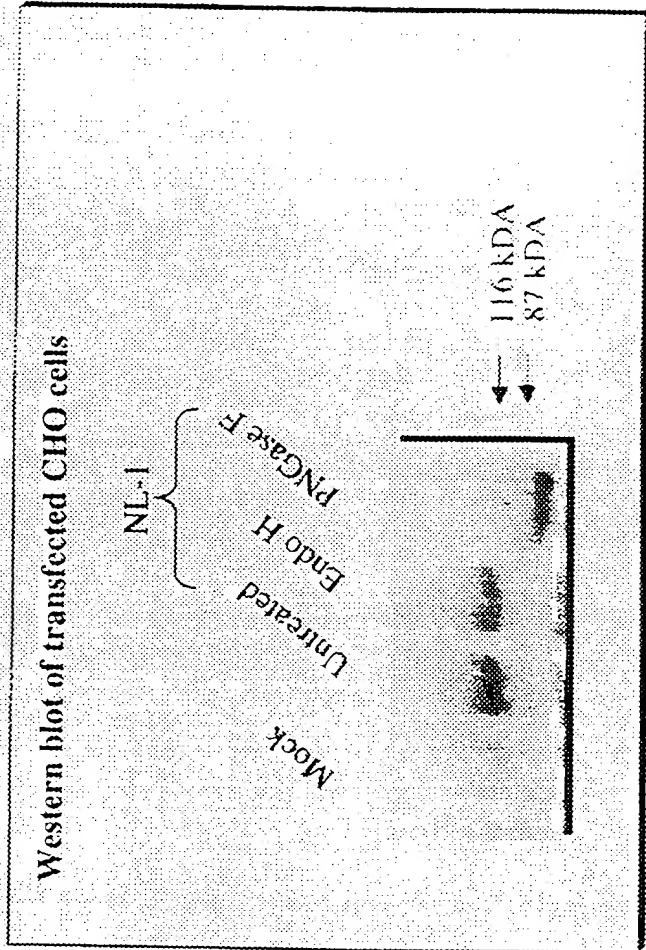
# Structure and expression of NL-1



Northern blot



Western blot of transfected CHO cells

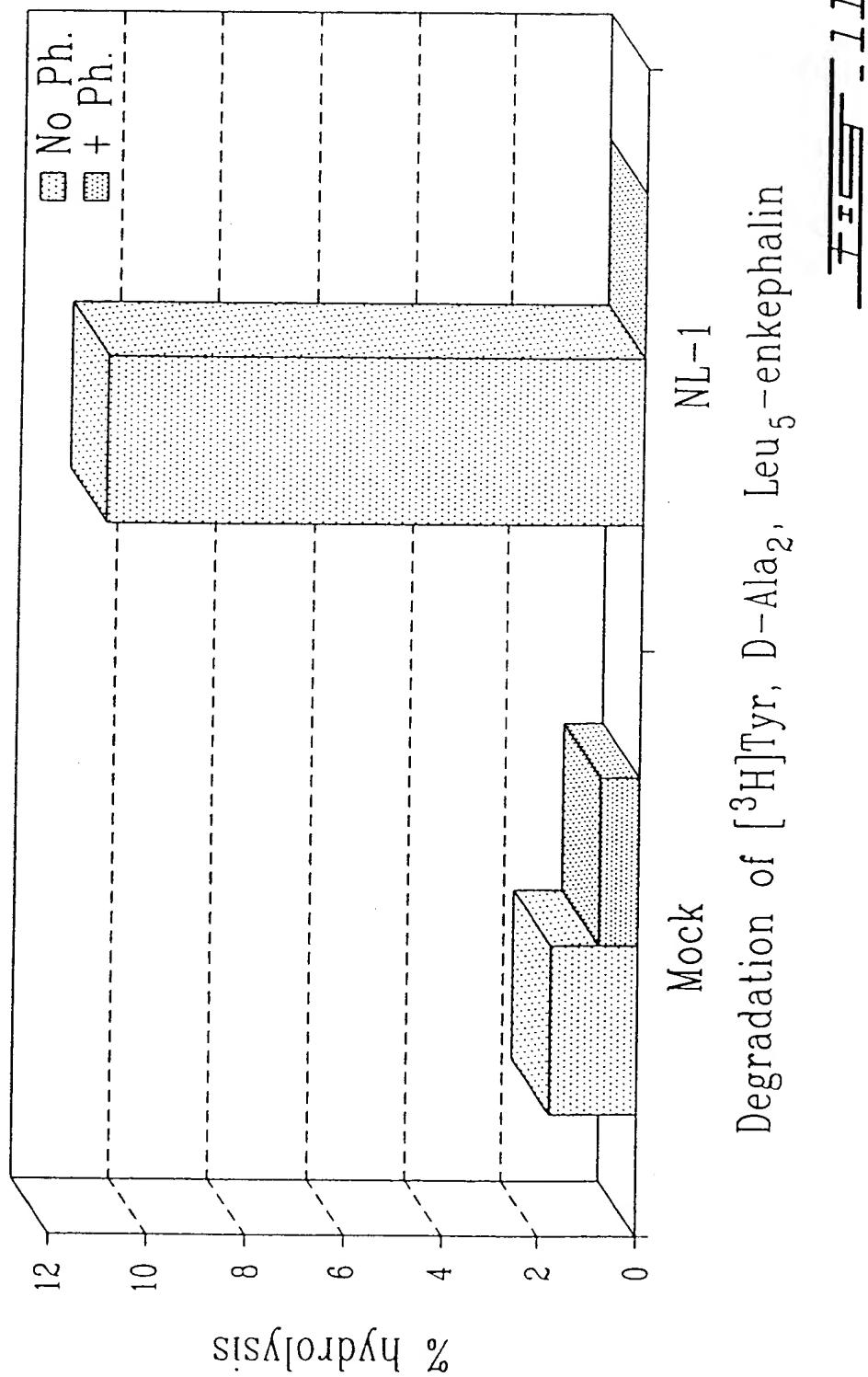
← 116 kDa  
→ 87 kDa

FOURTY EIGHT "SIXTY EIGHT"

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Enzymatic activity of NL-1

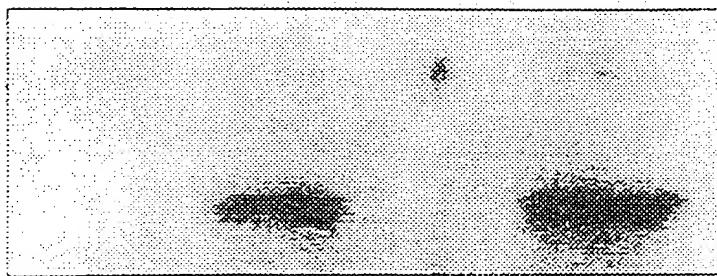


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MOCK

NL-3

CTL NL-3



~~FIG~~ - 12